

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGCTGTGATCCATGCACAAGGC~~GGGG~~CTGCTAGGCCCTC
TGTGCCCCGGCTTGGAAATTGGCTGCGGATGGCAGCTCCGGATGACCCGCCGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGCCCTCACCGACGGGATCGGCTTCGCCATGCCCGGC
GTTTGGCCCAAGGACGGGCCATGTGGTCGTCA~~G~~CAGCAGGGAAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGAGGGCTGAGCGTGA~~C~~GGGACCGTGTGCCATGTGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCACGGCTGTGAAGCTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGCAACCCCTTCTGGAAAGCATAATGATGTC~~A~~CTGAGGAGGT
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCA~~G~~CCCTGTGATGACA~~A~~AGGAGTGGTGC
AGAAATGGAGAACGAGGAGGGCTCAGTGGTGA~~T~~CTGCTTCATAGCAGCCTTCAGTC
CATCTCTGGCTTCAGTCCCTAACATGTCA~~G~~TAAAACAGCCTGCTGGC~~T~~GACCAAGACC
CTGGCCATAGAGCTGGCCCAAGGAACATTAGGGTGA~~A~~CTGCCTAGCAC~~T~~GGACTTATCAA
GA~~C~~CTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAGCATGAAAGAACCC
TGCGGATAAGAAGGTTAGGCAGGCCAGAGGATTGTGCTGGCATGTGTCTTCCTGTGCTCT
GAAGATGCCAGCTACATCA~~T~~CTGGGAAACAGTGGTGGTGGTGGAGGAACCCGTC~~CC~~GC
CTGAGGACGGGAGACAGCCCACAGGCCAGAGTTGGCTCTAGCTCTGGTGTGTTCC~~T~~G
ATTCA~~CC~~CACTGGC~~TT~~CCCACCTCTGCTCAC~~TT~~ACTGTTCAC~~CT~~CATCAAATCAGTTCT
GCCCTGTGAAAGATCCAGCCTCCCTGCGTCAAGGTGGCGTCTACTCGGGATTCCTGCT
GTTGTTGTGGC~~TT~~GGTAAAGGCC~~CC~~CTGAGAACACAGGACAGGCC~~T~~GCTGACAAGGCT
GAGTCTAC~~TT~~TGGCAAA~~G~~ACCAAGATATTTTCTGGCCACTGGTGA~~A~~TGTGAGGGTGA
TGGGAGAGAACGGAACTGGAGTGGAA~~G~~GGAGCAGAGTTGCAAA~~TT~~ACAGCTTGCAAA~~T~~GAGG
TGCAAATAAAATGCAGATGATTGCGCGCTTGA~~AAA~~AAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS
SRKQQNVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGGSVVIVSSTAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GGCCCTGAGCTCGCCTCGGCCGATAGCGCATCGAGAGCCTCGTCGAGGACCAAGCGGC
CAGGGGGCCGGCGAAAGGAGGATGAGGGGCGCAGCAGCTGCTGACCCCTGAGAACCGAGTGGC
GCGCTGGAGGAGGAGAACCGAGACTTCTGGCTCGCTGGAGGAGCCCATGGAGCAGTACAAACCTGC
AGAGGACCCGGCTCGTGAGCAGCAGGGAGAGATGGTGGACTCGCGCTGGGTTAGACTGGTGGCG
CCAGGCTGGGGGGCTCGCGCTCTGAATGCCCTGCCCTCGGGTCTTTGTGCTCACCTCATAC
AGCCCCCTGGGGGGTGCACGCCATGTGCTGGCATGGTGCCTGCTGCTGCCCTGGAGATG
AAGTTGGCTGAGCAGAGGGAGAGCAGGTGACAATGGCAGGGAGGCTGAGCTGACTGGTACT
GAGGTGAAACAGGCTGGGAAGTGGCTCTCACTGCTTCAAGGGAGGAAGAGGAGGAGGAGGCC
CAGCGGACCTACACCTGCGCAGAAATAGGATCAGCAACTCAGTCAGAGGGCGGGGCCAGCC
GGAGTCTGCAGAGAGGAAGGGCCAGAGCTTGAGGAGTTGGATGCAGCATTCCAGGGTCC
AGAGCAGTTGGTGGAGCAAGGCCAGTTCAGGCCAGCAGTCCGGCATCGAGCTTACGGCAG
GCCGCTGGGGCCAGGCCAGCAGAACGATCCGGGAGCTGGTATCACATCGCAGTAAGGGAGGCTTA
TTGGCAGACTGGTCCGCACAGGAGCCTCAGGGCTTAACCCGAGCACAGCAGCTATCGG
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGAGCT
CGAGGGCAAGGAGCTCCAGGATGCTGGAGCGGTCTCGCTCAGGGCTCAGGGCAGGGTCTG
CGGGAGGAGCTGGAGCTGGAGCTGGTCAAGGGAGAACGAGCTTACGGAGGGCTGGTCACTGCG
GCCAGAGTGTAGAAGGCAGTCTCAGGAGCTGCAGGCCAGCTGCAGCTCATGGCAGCAGCAGGACA
GCTGCAGAGGCCGCTTCGCAGGAGACGGAGCAGAACGAGCTGGAGCAACAGCAGAACGAGGAA
AGCACCGGTCAAGGAGCTGGAGCTGAAGCATGAGAACAGCAGAACAGTCTGGAGATTAAAGCGAA
GAGATCGCCCTCCAGAGGAAGGGCGCAGTGGCAGCAACGGCTGTGGTCAAGCTGGAGAC
GCCAGAGATTAGGAGCAGAACAGGAGCTGGTCAAGGGAGATGGAGGGTCTACAGCAGGGCGG
CGCTGGAGGAGCTGGGGAGGAGCTCCACAAGCGGGAGGCCATCTGGCAAGAAGGAGGCCATG
CAGGAGAACGAGGGCTGGAGAGCAAGGCCCTGAGATCACCGAGGCCCTAACAGGAGACATCGCG
AGTGTCCAGGGCTGGAGCACCTGGAGAGGAGCTGGCAAGAAGAGCGGGCAGCTGGCAGGGCA
GCCGCCAGGCCAGCAGCACATGCCGGGGAGATCGACAGCCTGCGCAGAGGACTCGCTGCTC
AAGCAGCGCTGGAGATGACGCCAACGCTGAGGAGGGACTCTGCTGCTCCCCGAGGAGGCC
GCTGTTCCAGTGGATGCCATGAGGCCCTGGATCTGGCAAGTCTGGTCAAGTATAAGAATGAGGCCATCA
CATGCCGCCAGGGCTGGCTCGGGGCTCACGGCTCGTCTGGCACTGGAGATGAACCTCATGGC
AAAGCTCAGTACCTCTCATCTCAGAGACAGAGGCCCTCTCTGCAAGTATTTGACAAGGTGGTGAC
GCTCCAGGGAGGAGCAGCACAGCAGCAGATTGCTTCTGGAGATGCCAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGGGCAGGCCCTGGAGATGGACGCCAGTGC
CTGCAGCAGAGGAGCACAGCAGAACATGCACTGCTCTGGCAGCAGAGTCTGGAGACCCACTGGTGA
AGGGTAGCAGACAGCAGGGAGCAGTATGAGGCCGGATCTAACAGCTCTGGAGAAGGAACCTGGCCCT
ACATGTGGATAAACCGAGGACTAACAGAACGAGCTGGGCTGTGGAGACCTGCTGGAGCAGCGGG
GGGGAGAGAGGGAGCTGTCTGGAGGGCAGACAGGCCCTGGAAATGAAGATGAGCTCCACCTG
ACCCAGCTCTCTGGCTCTCCCCCTCACTGGGGGGCCCCCGCACCCGGGAGGAGACGCCGGACT
TGGTCCACGCTCGTACCCCTGACCTGGAAACGCTCGAGCCCTGTTGAGGAGCAGGGTCCCC
GAGGAAGCTGGAGGAGGCCGGGGCTGGAGGCCCTGGTGGGGGGGGTGCCTCTGTGGGTGAGGCC
CCTGGCTGGAAACTTGGGCTTGTCTGGAGGCCGGGGAGCTGGAGGAGACTCCGAGCCT
TTGATGTCCGAAAACCCCTGTAAGCCCTGGGGCAGACCCCTGCCCTGGAGGAGACTCCGAGCCT
GCTGAAAGGGCAGCTGCTGTTTGTCTCTGTAAGGGCAGTCTTACCCACACCTAAATCCGAG
CCCTCATCTGACCCCTCACTGGGATCAACAAATTGGGCCATGGGCAAAAGAAGACTGGACCCCTCATTT
AACAAATAATATGCAAATCTCCACCAACTTACCTTCCATGAAGCTGTGTTACCCATTGCGCTTGT
TCTTGCTCGAATCTCAGGACAATTCTGGTTCAAGCGTAATGGATGTGCTTGTAGTTCAAGGGTTG
GCCAAGAATCATCACGAAAGGGTGGTGGCAACCAGGTGTGTTAAATGGCTTATGTATATAGGG
GAAACTGGAGACTTGGAGCTTAAACCATTTAATAAAAAAACCATTTAATAAAAAAATCTTGAAGGGAC

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465
<subunit 1 of 1, 830 aa, 1 stop
<MW: 95029, pI: 8.26, NX(S/T): 2
MEQYKLQSRTLREQQEEMVELRLRLELVPGWGGRLRNGLPPGSFVPRPHTAPLGGAHAHV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGLPERKGPELCLEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQGQLQRRLREETEQKRRLEAEMSKRQHVRKELELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVSLEQQQKIEEQKKWLQEMEKVLQORRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSLQALNEDIVRVSSRLHELEKELSEKSGQLRQGSAQSQQQIRGEIDS
LRQEKDSSLKQRLEIDGKLQRGSLLSPEEERTLFQLDEAIEALDAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSSETRALLCKYFDKVTLREEQHQQQIAFSELEMQLEEQQR
LVYVLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQRSDHLGEGGLADSRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEKRSLCSEGRCQAPGNEDELHLAPELLWLSPTEG
APRTTRETRDLVHAPLPLTWKRSSLCEEQGSPEELRQREAAEPLVGRVLPVGAEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTGGAACGATGAGGCCACGATGCTGCATCTGGCTTTGTCTGCT
GGATAACAGTCCTCCCTCCAGTGTCAAAGGAACTACAGACGCTCTGGCTCAGGA
CTGTGGCTGTGCCAGCGACACCAGGTGTGGGAACAAGATCTACAACCCCTCAGAGCAGTG
CTGTTATGATGATGCCATCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTGAGCTCTGCTGTCCCAGTCTTTGGCCCCAGCAGAAGTTCTTGTG
AAGTTGAGGGTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCGGAGCTGTAC
CAGGAACAGGAGGGCACGTCTGTACCCAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACCTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTGGAGAGGGAGCCAGCTGGGATGGC
CAGACTTCAGGGGAAGAATGCCITCCTGCTTCATCCCCTTCCAGCTCCCTCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCACATTACCATCT

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLLQCSKGTTDAPVGSGLWLQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSCTRNRRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCCCACGCGTCCGCCAACCGCTCCGGGTGCCACTCGCGCAGCGCTCCGGGCTTCCTCT
TTTCCCTCCGACGCGCACGGCTGCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCACCTCCGGAGAGGAGCGAGGCCGCCAGGGTGGCCCCGGGGCGCGTCTGGCTCG
GAGAAGCGGGGACGAGGCCGCCAGGATAGCGACTGAGGGCGACGCCGACTGACGCGAGTT
GGGGCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCG
GTGTGCGGCCAGGCGGAGCGCGCAGGTGGGCTGGGTGTTAGTGGTCCGCCACCGGGG
TCGCGGCCCGGCCAGGATGGCGCTGGCAACCCGGGCCGCCGCCCTGCTACCCCTG
CGCCCGCTGCGAGGCCGCCGCTCCGGCCCGCCCTGCGCTCATGGACGGCGCTCCGGCTG
GCGGCCGCCGCCGCCGCCGGCTGTGAATGCGACTCGCCCTCGGCCGCCCTCCCCGCC
GCCCGCCGGGACGTGGTAGGGATGCCGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCTGGTCACCTGCTGCCGTATGGTGGCTGTGAGTCGAGCATCCGCTGGAG
AAGCTGGCCAGGCCAGCAGCAGCCGGCCAGGAGAAGCGTGAGCACGCCACTGGGACGG
CCCGGGGGGGGTGAACGAGCTGGGCCGCCGGCGAGGGACGAGGGCGGAGCGGGGGACT
GGAAGAGCAAGAGCGGCCGTGGCTCCCGGCCGTAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCCAGGGCGGGGGGCCAAGGCGGGGATCTGAGGTCCGGCCCCGGGGACAC
CCCGCAGGCCAGCCACCGAGGAGTACGTGTACCGGACTACCGTGGCAAGGGCTCGTGGACAG
AGCGGCTTCGTGTACCGATCGGGAGAAGTTCGCCGGGCCCTCGGCCCTGCCGTGCT
GTGCACCGAGGAGGGGCCGTGCGCGCAGCCCGAGTGGCGAGGCTGCACCCGCCGTGCA
TCCACGTCGACACGAGCCAGTGTGCTGCCCGAGTGCAGGAGAGGAAGAACTACTGCGAGTT
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTGTTGCTCCATGCGAGAGGTGTCGCTG
TGAAGCCAACGGTGAGGTGCTATGCACTGAGCTGAGGTGCTCCAGACGGAGTGTGAC
CTGTGTACGAGCCTGATCAGTGTGCTCCATCTGCAAAATGGTCAAACACTGCTTGCAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGCAGGGCATGTGCAGAGACATGAATGCA
AAATGTAGACGCTTCCCAGAACACAAACTCTGACTTTCTAGAACATTTACTGATGTGAA
CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTGAGGAAATAATGGAAA
TTGTTGGTACTTTCTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTC
AAAACATCAACAAGAACCTTGGGCATAAAATCCTCTCTAAATAATGTGCTATTTCACAG
TAAGTACACAAAAGTACACTATTATATCAATGTATTTCTATAATCCCTCATTAGAG
CTTATATAAGTGTCTATAGATGCAGATTAAAATGCTGTGTTGCAACCGTAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKEHATRDGPGRVNEL
GRPARDEGGSGRDWKSKSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALA
AAAQDAIGPELAPTPPEPEEYVYPDYRGKGCVDESGFVYAIKEKFAPGPSACPCCLCTEEGPL
CAQPECPRHLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFATAVAPIAGREVKTDECTICHCTYEEGTWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCA**TGAGCGCGTATTACTGCTGGCCCTCCTGGGTTCATCCTCCCAC**
TGCCAGGAGTGCA**GGCGCTGCTGCCAGTTGGGACAGTTCAGCATGTTGAAAGGTGTCC**
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCACAGCGCTGGGTCAGGA
CACGTTGATGTCATTGAGAGCGGACCCAAGTGAGGCTGGTGCCTCCAAGGGTGCACGG
AGGCCAAGGACCAAGGAGCCCCCGCTCACTGAGCACGGATGGGCCCCGGCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTATGG
AAGGCTGTCTGGAGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGACACAGGAATTGGGCCGTGGTATGACTGAGA
ACTGCAATAGGAAAGATTTCTGACCTGTATCGGGGGACCACCATATTGACACACGGAAAC
TTGGCTCAAGAACCACTGATTGGACACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
GTGTCAGGAGAGCCTGCTGCTCATAGATGTAGGACTCACATCAACCCCTGGTGGGACAAAAG
GCTGCAGCACTGTTGGGCTCAAATTCCAGAAGACCACCATCCACTCAGCCCCCTGGG
GTGTTGTCCTCTATACCCACTTCTGCTCCTGCCACCTGTGCAATAGTGCAGCAGCAG
CAGCCTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACCGCAGTGT
CTACCTGTGTGCAGCCCCCTGGAACCTGTCAGTGGCTCCCCCGAATGACCTGCCAG
GGGCCACTCATGTTATGATGGGTACATTCACTCTCAGGAGGTGGCTGTCCACCAAAAT
GAGCATTCAAGGGCTGCGTGGCCCAACCTTCCAGCTTGTGAAACCACCCAGACAATCG
GGATCTCTCTGCCGTGAGAACCGTGATGTGCAAGCTCTGCCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTGCCCTCTGCT**AACTCTATTACCCCCACGATTCTCACCGCTGCTGA**
CCACCCACACTCAACCTCCCTGACCTCATAACCTAATGCCCTGGACACCAGATTCTTC
CCATTCTGTCCATGAATCATCTCCCCACACACAATCATTCACTACTCACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGACTTGCCTATGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCCTGTCCCTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847
><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
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ESGPQVSVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTEEICPKGTTCHYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVQVCQETL
LLIDVGLTSTLVGPKGCTVGAQNSQTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSSGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPAPASQHEGGGAEGLESLTWVGVLALAPALWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACCGCGCCGGCTGCCCTCCGGACCTCCGTAGCGCCTGCCCGGCCCTG
GCTCGCGCCTGCTCTCGCTTGCCTGCTCTCTAGAGCCGAGGGACCGGGTGGC
CTCGTCGCTCAGCCCCATTTCGGCAAAAGACTCGCTACGAGGATGTCAACCCCGTCTAT
TGTCGGGCCCCGAGGCTCGTGGCGGGACCTGAGCTGCTGGAGGGACCTGACCCCGTGT
CAGCTGGTCGCCCTCATTCGGCACGGCACCGCTACCCCAAGCTCAAACAGATCCGAAGCT
GAGGCAGCTGCACGGGTTCTGCAGGGCCGGGTCAGGGATGGCGGGGCTAGTAGTACCG
GCAGCCGCGACCTGGGTGCAAGCGCTGGCGACTGGCTTGTGCTACCGGACTGGATGGAC
GGGCACTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCCCTGCGTCTGGCCTCGCT
CTTCCCGGCCCTTTCAGCCGTGAGAACTACGGCCCTGCGGCTCATCACCAAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCTTCTGCAGGGCTGTGGCAGCACTACCAACCCCTGGC
TTGCCCGCCGCCGACCTGGCAGATATTGGAGTTGGACCTTCAAACAGTTAATGATAAACTAT
GAGATTTTTGATCACTGTGAGAAGTTTAATGAGTAGAAAAAAATGCTACGCTCTT
ATCACGTGGAAGCCTTCAAACCTGGACCAGAAATGCGAACATTTAAAAAGTTGCGAGCT
ACTTTGCAAGTGGCAGTAAATGATTAAATGAGATTAACTTCAGTACGCTTTTACACCTG
TTCATTGACCTGGCAATTAAAGGTGTTAAATCTCTTGGTGTGATGTTTTGACATAGATG
ATGCAAAAGGTATTAGAATATTAAATGATCTGAAACATATTGGAAAAGAGGATATGGGTAT
ACTATTAAACAGTCAGTCAGCTGCACCTGGTTCAGGATATCTTCAGCACTTGGACAAGC
AGTTGAACAGAAACAAAGGTCTCAGCCAATTCTCTCAGTCATCTCCAGTTGGTCTG
CAGAGACTCTCTCCACTGCTTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAAC
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CTCGAACCTGTATTGGTCTTACCACTGTGAAATGCTAAAGCTCCAAAGAACATTC
GAGTGCAGATGTTAAATGAAAAGGTGTTACCTTGGCTTACTCACAAGAACATGTTCA
TTTATGAAGATCTGAAAGAACACTACAAGGACATCCTTCAGGTTGCAAACCAAGTGAAGA
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TTATATAAGAAAATCTCACACTGAGATAGAATTGTGATTTCATAATAACACTTGAAGAAGTGT
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TGAAAATAATATTGGTATTATGAAATATTGAACATTTCATAATAACACTTGAAGAAGT
TTTACTCTAGGAAGTCTCAAAAGACATCTTAAATTATTATGTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATGCAAGTTTCAATTCATTGCTTAGCTAACTTTTCTATTCTGT
CACTGGGCTCGATTTTATATTCTCATTATGAAATGTTGATCTTGGTTGTTGATT
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FIGURE 12

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400
><subunit 1 of 1, 487 aa, 1 stop
><MW: 55051, pI: 8.14, NX(S/T): 2
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RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAFLQGLWQHYHPGLPPPDVADMEFGPPVTNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNLDLNADLIQVAFFTCSDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMILLNEKVLPPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL
```

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCCGCCCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCCGCCACCGCGAC
TCGGCGCTCGCGCTCGCTCGACTCTCTCTCGCTCTGCTTTCAGGGCTGCCTGATAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCACTGGTACAGGAATTGAAAGTGTGGAACCTGTCTTGATCATTTAGGATTCCG
ATCAAGTGAACCCGAGATCGACTGGAGAAGAAAATTCAAGATGAAACAAACCATATGTGTTTTGACAAAAAA
TTCAAGGGAGACTTGGCGGTGCTCGAGAAATACTGGGAAGACATCCCTCGAGATCTGAAATGTGACACCGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGCTGAAATGACCGCAAGGAAATTGTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGAACCCCTGTCTGACTAGGTGCGGAGCTGTACCCAGTAGGCAAGATGCAACACTGC
ACTGCCAGGAGACTGAGGCCACCCCGCCCTCACTACAGCTGGTATCGCAATGTGATGACCCACTGCCAGGATT
CCAGAGCCAACTCCAGATTCTCGAATTCTCTTCCACTTAAACCTCTGAAACAGGCACCTTGGTGTCACTGCTG
TTCAACAGGAGCAGACTTGGGAGACTACTSCATTGCTCCAACTGACGCCAGGCTCGACCCAGGTGTGAGGAGCAG
AGATGAGAAGTCTATGATCGACAACTTGGCGGAATTATTGGGGGGTCTCTGGTGTCTTGCTGACTGGCCCTGA
TCACGTGGGCATCTGCTGTCATAAGACGTGCTACTTCATCAACAAATAACAGGATGGAGAAAGTACAAGA
AGCAAGGAAACAGAGATGAGTAACTACACCCGACTGACGCCAGGAGGGCGACTTCAGAACACAGTCTGTTG
TGATCTGAGACCCCGCTGGCGTGAAGGCCACAGAGCCGACCTGCACTTCTGCTAGAAACTCTCTGCTCAA
GGCAGGGAGAGCTGATGCACTCGACAGAGCTAGACACTCATTAGAAGCTTTCGTTTGGCCAAGTTGACCA
CTACTCTTCTACTTAAACAGCCACATGAAAGAATTCTCTCAAGATGACCCGGTAATAATTGGGGGG
GGAGGAAACATTGGTGTGGAGGATCTGGCTGAGAACCCCTGCTTGTCAAGGTTAACAGGTTAAGGAA
ACCTTCTCTTACTGGCTACTGCTAAATGCTACTGAAATTGCTTCTGTTCTGGTTTATTTAAATTT
TACATCTAAAGATTGCTCACGTTAAACGCCGCTGGGCCCTGTGAAGGCCAGCATGTTACCAACTGTCGTT
CAGGCCAGCACAGCACAGTGTGAGATGGCGAGGTGCTGGCAGCAGGCCACAGGCCATCCGGCGGAGACCA
GAAAAGGCTCTTACAGCNGCCCTATCTCATGGCCCAACAGAACCCACCCGGAGTTCTCTTCTAAAGGCTCTG
TGATCGGTGTGAGTGTCCATTGGAGAAAGCTTGGATCAGCATTTGTTAAACAAACAAACAAATCAGGAAG
GTTAAATGGTGTGGAGAAGGGATCTGGCTGAGAACCCCTGCTTGTCAAGGTTCAAGGTTCAAGGTTAACAGGAA
ACCTTCTCTTACTGGCTTACTGGCTACTGCTAAATGCTACTGAAATTGCTTCTGGTTTATTTAAATTT
TACATCTAAAGATTGCTAACAAACCTTAACTTAAAGGAAATTGTTAAATTTAAAGAAAATTCTTATTTAAACGTA
CATACATGTTAAATAACCTTAACTTAAAGGAAATTGTTAACTTAAAGTGAAGTCAACTGTTCAAGGTT
TGGAAATATCAATAATTAAGAGTATTTCACCGAAAGTCTCTCATGAGTGTGTTCTGTTCTTCT
CACACAAGTTTACCGCTTTCACAGGGAACTCATACTGTCACACATCAGACCATAGTGTGCTTAAAGGAA
TAAAGTCTCAGTAAAGCACTGTTGAAATCTGGCTCTCTCCTAAAGAAACCTCTCAGGTTAGCTTAACT
GCCCTCTCTGAGATGACTGGAGACTGTCAGGAGCAGTGTGCTGAGGCTCCAGTGTGCTTAAAGGCT
GCCATCTTGGCCCTGCGACTGGCTGTGCTTCCAGTGTGCTTCTCATGCTTGGCTCTGTCACAGCACAG
TCTCAGGTTGGGACTCAGGAGACTGGTGTCTTCTCATGAGTGTGCTTGGCTCTGTCACAGCACCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAACTGCTATTTTTTTTAAAGTTGTTAATTATTGTT
AAGATGTCATAAGGCCAAAGGCAATTGGAAATCAAGTGTGTCAGTAACTAAACATTTTAAAGAAAATTGGAT
CCCAGTCTCTTGGCCACAGAAAGGCCACAGGCCACAGGCCACAGGCCCTGTGCGCATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCAGGCCCTTAAAGAACCTGAGGTGGACGCCAGGTGAAGGCCCTGGGGAGAAAAG
TGAACGCCCTGAATCAAAAGCAGTTTCTAAATTGACTTTAAATTGTTCTATGCCGGAGACACTGCTCCATT
TGTGGGGGGAGACTTGGCAACACTGCAAGAGCCCTGTGTTCTCAAGAGCAGGTGTTCTCAGGCTCATGCCCT
GCCGCTGCTGGACTCAGGACTGAAGTGTGTCAGAAGCAGGAGCTGCTGAGAAGGGGACTCCACTGTGCTG
GAATGGCTCTCACTACTCACCCCTGCTTCAGCTTCCAGTGTCTGGGTTTTTATACTTTGACAGCTT
AATTGTCATCATGAGACTGTGACTTTTTACTGTAACACTTTGCCAGGCCCTGGAGGCC
GGAAATGCTCCAGCAGTGGCTCAGTGTGCTCCCTGGTGTGCTGCGCATGGCATCTGGATGCTTCACTGCAAGTTC
CCTCCATCATGGCACCTTGTGAGAGGGTAGGCTCCACCCACCTCAGGCTTGGGATTACGCTCCAGGCCCT
TCTGGTTGTCATAGTGATAGGAGGATGGCTTATGCCCCCTCTTACCTAAACCCCTACACTAGTGCA
TGGGAAACCGGACTGAAAAGTAGAGAGAAGTGAAGTAGACTGCTGGAAAGTAGCTGCTTACGCTTACACTAG
CGGAAAGGAAATACTCGTGTATTAAAGATACTGAATGTGACTCAAGACTCGAGGCCATACGAGGCTGTGATTCT
GCCCTTGGATGGATGTGCTGTCACAGATGCTACAGACTTGTACTAACACACCGTAAATTGGCATTTGTTAAC
CTCATTTAAAGCTCAAAAAACCCA

FIGURE 14

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFDFDNKIQGDLAGRAEILGKTSLIKWNVTTRDSALYRCEVVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, PI: 6.42, NX(S/T): 0

MHILVVHAMVLLTGPRAADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLPDLKLRM
IRSEVLRVLDAALQDLEPQQQLLFFVQSFGIPVSSMSKLLQFLDQVAHDPCQTLEQNIMDKNY
MAHLLEVQHERGASGGQTFHSSLTASLPPRDRDSTEAKPKKSSPEQPIGQGRIVGVQLRLVG
PEDDLAGMFLQIFPLSPDPRWQSSPRVALALQALQGELARVVGSPPEVPGITVRVLQD
ATLSSPHGGLAVMSMRHSFLACPLLRQLCQYRCVCPDTGFSSFLKVLLQMLQWLSDPG
VEGGPLRQLRMLASQASAGRRLSDVRGGLLRAEALAFRQDLEVVSSVTRAVIATLRSSEQ
CSVEPDLSKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSLLQEEEPLA
GGKPGADGGSLEAVRVLPGSSGLLWDLWEMLPDVPEVVSSCPDLQRLLFSRNRKGKQAQVPSFR
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRDFPSASLDFLWCACIHPVRIWQGRDQRTPQKR
REELVLVRQGPELISLVELIABAETRSQDGDTAACSLIQARLPLLSSCCGDDESRVKTE
HLGCIQQWGSVLRCCRDLQLLYLQLRPELVRPVEVLLHSEGAASSSVCKLGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVALHGRTHLNQFERQZNHL
SCFLHVGLLELLQPHVFRSEHQGALWDCLLSFIRLLNRYKSSRHAAFINKFVQFIIHKYI
TYNAPAAISFLQKHADPLHDLSDFNDSLVMKSLLAGLSPSRDRTDRLGDEEGEEESSAG
SPLLVSVSLFTPLTAEMAPYMKRLSRGQTVEDLLEFLVSDIDEMSRPPEIISFFSTNLQRL
MSSAECCRNLAFSLALRSMQNSPSIAAFLPTFMYCLGSQDFEVVQTALRNLPYALLCQE
HAAVLHRAFLVGMYQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,

665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCCCATGCAGCCTCGGCCCCCGGGGCCCGCCGCACCCGAGGAGATGAGGCTCCGC
AATGGCACCTTCTGACCGTGTGCTCTCTGCTCTGTGCGCTTCCTCTCGCTGTCTGGTA
CGGGCACTCAGCGGCCAGAAAGGCAGCTTGAGCTTACACGGGAGTTCTGGCGC
TGCAGATCGGTTGCACCGAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGGCGTGTGAGAAAGGCAGGGCTGCGAGACGGAGACCGCAA
TCGCACCTGGGGCGCCTAACAGAGGCCCGATTGAAGCGTGGAACCGCTCACCCGGC
ACGTGCTGCACCTGCCCATCGTCTCCATCACCTGCCAACCTGCTGGCCAAGGAGAGCAGT
CTGAGGCCCGCGGTGCGCTGGGCCAGGGCGCACCCGAGTGTCTGGTGTGGATGGGCATCCC
GAGCGTGGCGCGAGGTGCACTCGTACTGACTGACACTCTGÇACTCGCTCATCTCGAGC
TGAGCCGAGGAGAAGGAGGACTCGGTATCGTGTGCTGATCCCGAGACTGACTCACAG
TACACCTTCCGGACTGACAGAGAACATCAAGGCCCTGTTCCACGGAGATCCATCTGGGCT
CCTGGAGGTCACTCACCCCTCCCCCATCTACCTCCGACTCTCCGGCCTCGAGAGTCT
TTGGGGACCCCAGGAGAGTCAAGTGGAGGACAAACAGAACCTCGATTACTGCTTCTC
ATGATGTACCGCAGTCACAGGACATCTACTACGTGAGCTGGAGGATGACATCGTGGCAA
GCCCAACTACCTGAGCACCATGAAGAACTTTCGACTGAGCACCTCAGAGGACTGATGTA
TCCTGGAGTTCTCCGACTGGCTTCATTGGTAAGATGTTCAAGTGCCTGGACCTGAGCCTG
ATTGAGAGTTCACTCTCATGTTCTACCGGACAAGCCCATCGACTGGCTCTGGACCATAT
TCTGGGGTGAAGGTGCAACCCCGAGAAGGATCGCAAGGACTGTGACCGCAGAAAGCCA
ACCTCGGGATCGCTTCAACCGTCCCTTCCAGCACGTGGGACTCACTCCTCGCTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTGGAAAGCAGGCCGTGCGGAAGGAGCATGT
GAACCCCGCAGCAGAGGTGAGCACGAGCCTGAGACATACAGCACCTCCACCTGGAGAAC
CCTACCTGGCGAGGACTTCTGGGCTTCACCCCTGCCGCGGGGACTTCATCCGCTTC
CGCTTCTCCAACCTCAAGACTGGAGCGTTCTTCTCCGCACTGGGAACATCGAGCACCC
GGAGGACAAGCTTCAACGTCTGGAGGTGCTGCCCTCGACAACCCCTCAGTCAGACA
AGGAGGCCCTGCAGGAGGGCCGACCGCCACCCCTCCGTACCCCTGGAGCCCGACGGCTAC
CTCAGATCGGCCCTCTACAAGGGAGTGGCAGAGGGAGGGTGGACCCAGCCTCGGCC
TCTGGAAAGACTCGGCCCTCTCGATCCAGACGACTCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCTGAAAAAGGCCATAGCTGGGCTTCTGAGGGTACCCGTGGCCAGCCCTGAA
GCCACATTCTGGGGTGTGCTACTGCCGTCCCGAGGGCCAGATAACGGCCCGCCCAA
AGGGTTCTGCCCTGGCTCGGGCTTGGGCCGCTGGGTCCGCCCTGGCCGGAGGCCCTA
GGAGCTGGTGTGCTGCCCGCCGCCGGGGAGGGAGGGCAGGGGGCCCCACACTGTGCC
TGAGGCCCGAACCGTTCGACCCGGCTGCCAGTCAAGGCCCTGGTGTGGGTGATTCTGAGCGAG
TTGGGCCCGCCGTCTGGCCGAACACTGGAATGCACTATACCTTATGTGCTGTGTT
TTTATTCTGGATACATTGATTTTACGTAAGTCCACATATACTTATATAAGAGCGT
ACTTGTAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
MRLRNGTFLTLLLFCCLCAFLSLSWYALSGQKGDVVDVYQREFLALRDRLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRGDGNTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVIAE
TDSQYTSAVTENIKALFPTEIHGLLEVISPSPHFYPDFSRLRESFGDPKERVRWRTRKQNLD
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILEMFYRDKPIDWLDDHILWVKVCNPEKDAHKCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDQDFGKQALRKEHVNPAPAEVSTSLKYQHFTLEKAYLREDFFWAFTPAAAGD
FIRFRFFQPLRLERFFFSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVVWILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515